

FIGURE 1

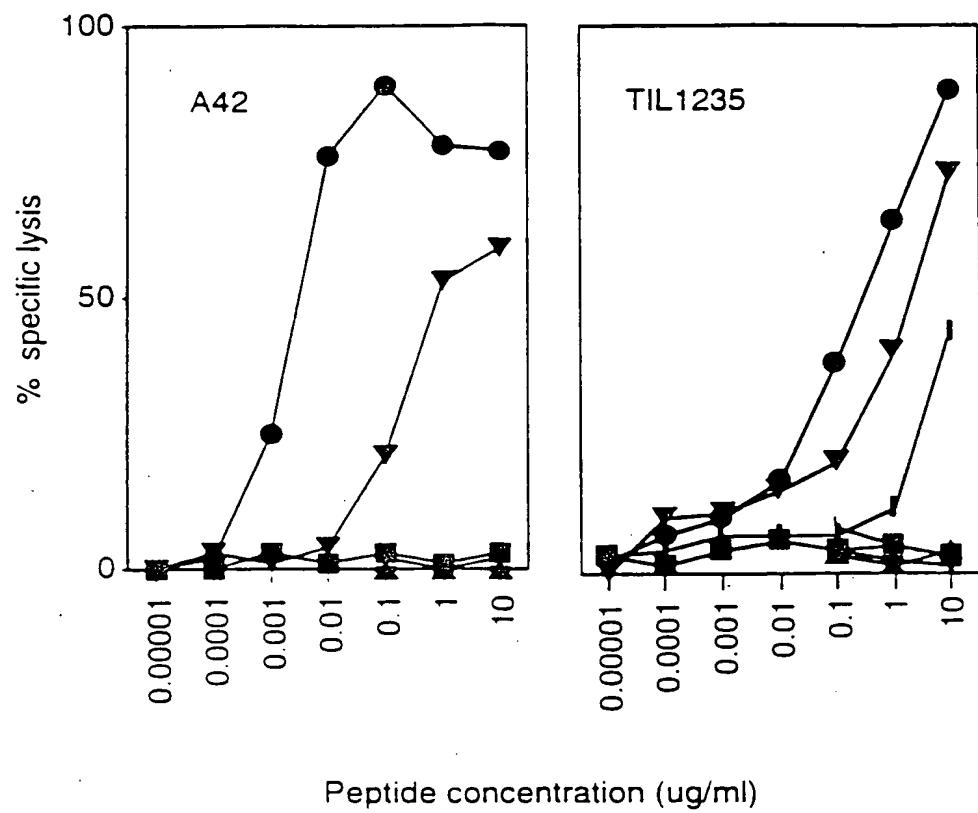


FIGURE 2

FIGURE 3A

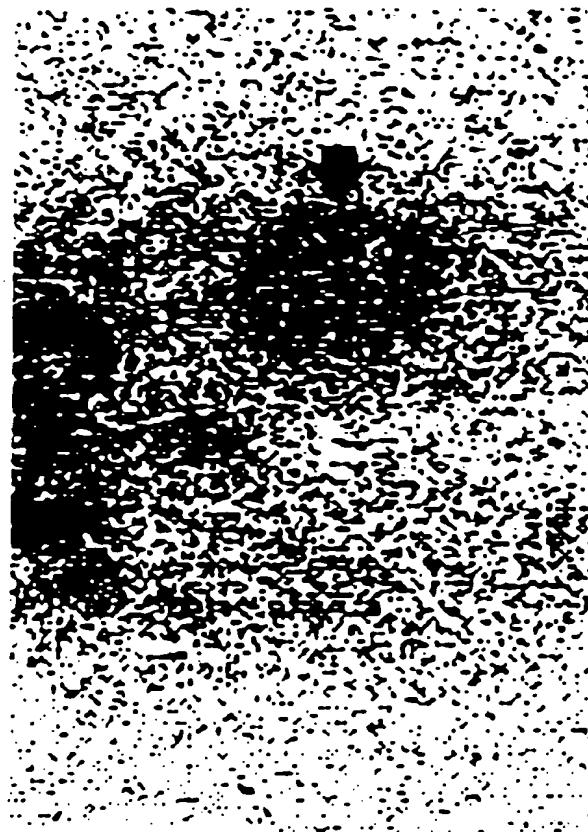
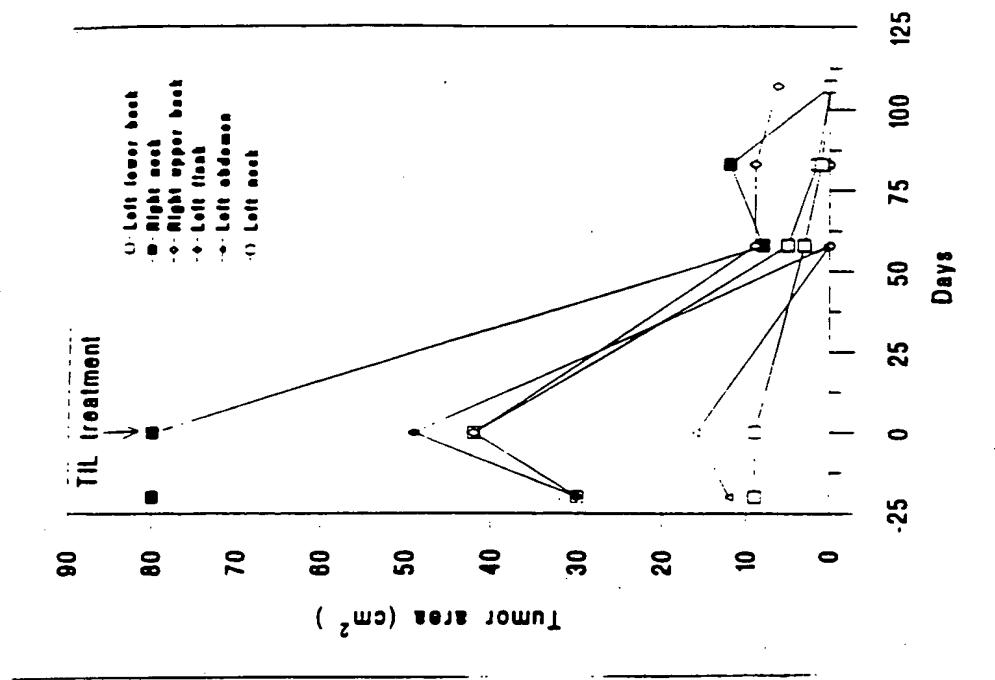


FIGURE 3B



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GTCGACGGCC	ATTACCAATC	GCGACCGGGGA	AGAACACA <u>AT</u>	40	
<u>GGATCTGGTG</u>	CTAAAAAGAT	GCCTTCTTCA	TTTGGCTGTG	80	
ATAGGTGCTT	TGCTGGCTGT	GGGGGCTACA	AAAGTACCCA	120	
GAAACCAGGA	CTGGCTTGGT	GTCTCAAGGC	AACTCAGAAC	160	
CAAAGCCTGG	AACAGGCAGC	TGTATCCAGA	GTGGACAGAA	200	
GCCCAGAGAC	TTGACTGCTG	GAGAGGTGGT	CAAGTGTCCC	240	
TCAAGGTCA	GA	TAATGATGGG	CCTACACTGA	TTGGTGCAAA	280
TGCCTCCTTC	TCTATTGCCT	TGAAC	TTCCC	TGGAAGCCAA	320
AAGGTATTGC	CAGATGGGCA	GGTTATCTGG	GTCAACAAATA	360	
CCATCATCAA	TGGGAGCCAG	GTGTGGGAG	GACAGCCAGT	400	
GTATCCCCAG	GAAACTGACG	ATGCCTGCAT	CTTCCCTGAT	440	
GGTGGACCTT	GCCCATCTGG	CTCTTGGTCT	CAGAAGAGAA	480	
GCTTTGTTA	TGTCTGGAAG	ACCTGGGCC	AATACTGGCA	520	
ATTTCTAGGG	GGCCCAGTGT	CTGGGCTGAG	CATTGGGACA	560	
GGCAGGGCAA	TGCTGGGCAC	ACACACCATG	GAAGTGA	600	
TCTACCATCG	CCGGGGATCC	CGGAGCTATG	TGCCTCTTGC	640	
TCATTCCAGC	TCAGCCTTCA	CCATTACTGA	CCAGGTGCCT	680	
TTCTCCGTGA	GGGTGTCCCA	GTGCGGGCC	TTGGATGGAG	720	
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760	
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800	
GACCTCTCCT	ACACCTGGGA	CTTGAGAC	AGTAGTGGAA	840	
CCCTGATCTC	TCGGGCAC	TTGTCACTC	ATACTTACCT	880	
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920	
GCCATTCC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960	
GCACCACAGA	TGGGCACAGG	CCAAC	TGCAG	AGGCCCCCTAA	1000
CACCA	CAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080	
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120	

FIGURE 4

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA 1440
AGAGACAAAGT CCCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480
TTCCTTTCC GTCACCCCTGG ACATTGTCCA GGGTATTGAA 1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560
ATGCATTGGA GCTGACTGTG TCCTGCCAAG GCAGGGCTGCC 1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640
CCCCCTGCCA AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAAC TGAAGGGTGG 1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCCTCTACC 1960
CCGCATCTTC TGCTCTTGTG CCATTGGTGA GAACAGCCCC 2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT 2120
ACTCAGAGCC TGAAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160
AAAAAAAAAA AA 2172

FIGURE 4 (continued)

FIGURE 5A

1	MDLVLKRCCLL	HLAVIGALLA	VGATKVPRNQ	DWLGVSRLQR	TKAWNRLQY
51	EWTEAQRILDC	WRGGQVSLKV	SNDGPTLIGA	NASFISIALNF	PGSQKVLPDG
101	QVIWVNNTII	NGSQVWGGQP	VYPQETDDAC	IFPDGGPCPS	GWSQKRSFV
151	YVWKTWQYQW	QFLGGPVSGL	SIGTGRAMLG	THTMEVTYH	RRGSRSYVPL
201	AHSSSAFTIT	DQVPFSVSVS	QLRALDGGNK	HFLRNQPLTF	ALQLHDPSGY
251	LAEADLSYTW	DFGDSSGTLL	SRALVVHTY	LEPGPVTAQV	VLOAAIPLTS
301	CGSSPVPGTT	DGHRPTAEAP	NTTAGQVPTT	EVVGTTPGQA	PTAEPSGTTS
351	VQVPTTEVIS	TAPVQMPM	STGMTPEKVP	VSEVMGTTLA	EMSTPEATGM
401	TPAEVSIVVL	SGTIAQVTT	TEWVETTARE	LPIPEPEGPD	ASSIMSTESI
451	TGSLGP LL DG	<u>TATLRLVKRQ</u>	VPLDCVLYRY	GSFSVTL	QGIESAEIQL
501	AVPSGEGDAF	ELTVSCQGGL	PKEACMEISS	PGCQPPAQL	CQPVLPSPAC
551	OLVLHQIILKG	GSGTYCLNVS	LADTNSLAVV	STQLIMPGQE	AGLGQVPLIV
601	GILLVLMMAVV	LASLIYRRRL	MKQDFSVPQL	PHSSSHWLRL	PRIFCSCPIG
651	ENSPLLSGQQ	V			

FIGURE 5B

Pmel17	M	-----	V	-----	Q	-----	P	-----	VPGILLT	-----	LLSGQQV
ME20	M	-----	V	-----	Q	-----	L	-----	-----
gp100	M	-----	V	-----	Q	-----	L	-----	-----
CDNA25FL	M	-----	F	-----	Q	-----	L	-----	-----
CDNA25STR						Q	-----	L	-----	...	PPQWAAGLSTLI
	1	162	236	274	588					649	

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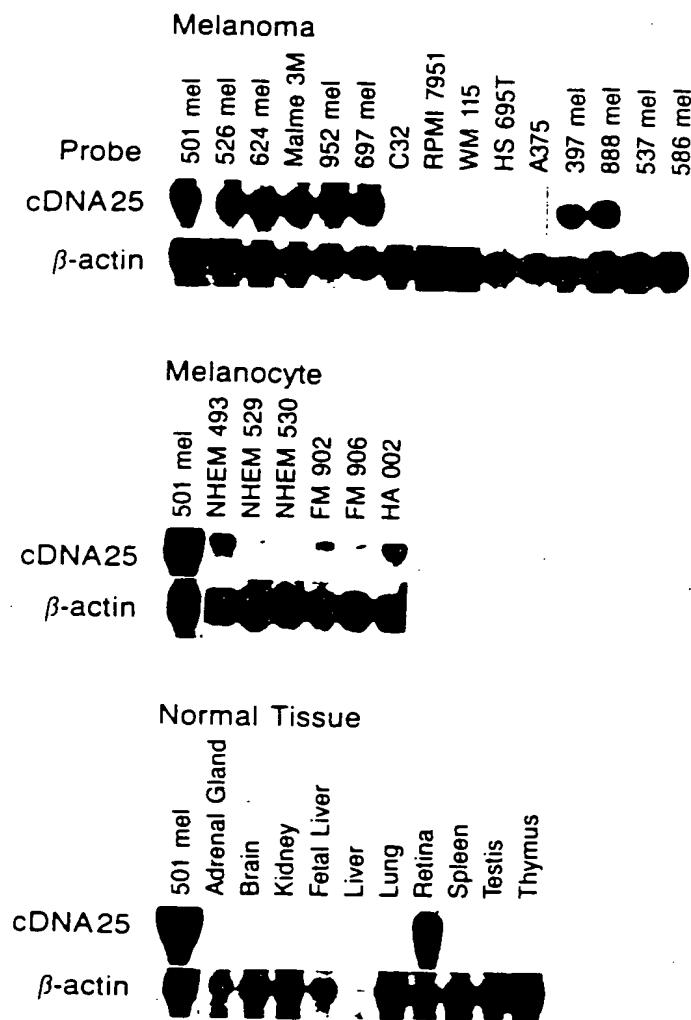


FIGURE 6

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